

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Malcolm Whitman and Xin Chen

(ii) TITLE OF THE INVENTION: METHODS AND REAGENTS FOR MODULATING
TGF-BETA SUPERFAMILY SIGNALLING

(iii) NUMBER OF SEQUENCES: 18

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Clark & Elbing LLP

(B) STREET: 176 Federal Street

(C) CITY: Boston

(D) STATE: MA

(E) COUNTRY: USA

(F) ZIP: 02110

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette

(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: DOS

(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: 27-MAY-1998

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/047,991

(B) FILING DATE: 28-MAY-1997

(viii) ATTORNEY/AGENT INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1658 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xenopus Smad2 coding region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGTCGTCCA TCTTGCCTTT CACCCCGCCA GTAGTGAAGC GCCTGCTAGG ATGGAAGAAG 60
TCTGCAAGTG GCACCACAGG AGCAGGTGGC GATGAGCAGA ACGGACAGGA AGAGAAGTGG 120
TGCGAAAAAG CGGTAAAGAG CTTGGTGAAA AAACCTGAAGA AAACGGGACA ATTAGACGAG 180
CTTGAGAAGG CGATCACGAC GCAGAACTGC AACACGAAAT GCGTAACGAT ACCAAGCACT 240
TGCTCTGAAA TTTGGGGACT GAGTACAGCA AATACCATAG ATCAGTGGGA TACCACAGGC 300
CTTTACAGCT TCTCTGAACA AACCAGGTCT CTTGATGGTC GACTCCAGGT GTCTCACCGT 360
AAAGGATTGC CGCATGTTAT CTACTGCAGA CTGTGGCGCT GGCCAGACCT GCACAGTCAT 420
CATGAAGTGA AAGCAATCGA AAATTGTGAA TATGCTTTTA ACCTTAAAAA AGATGAAGTT 480
TGTGTCAATC CATAACATTA TCAGAGGGTG GAGACACCAG TTTTACCACC TGTATTAGTT 540
CCACGGCACA CGGAAATCTT GACAGAGCTG CCACCTCTTG ATGACTACAC GCATTCCATT 600
CCAGAAAACA CTAATTTTCC TGCAGGGATT GAACCTCAGA GCAATTATAT TCCAGAAAACA 660
CCACCTCCTG GATATATTAG TGAAGATGGA GAACTAGCG ATCAGCAACT TAACCAAAGC 720
ATGGACACAG GGTCACCAGC TGAGCTGTCT CCGAGTACAC TTTCTCCAGT CAACCACAAT 780
CTCGATTGTC AACCTGTCAC CTATTCGGA CCTGCTTTT GGTGCTCTAT AGCATACTAC 840
GAACTGAATC AGCGAGTAGG AGAAACTTTC CATGCATCGC AACCATCGCT TACCGTGGAC 900
GGCTTTACGG ACCCCTCAAA CTCTGAAAGG TTCTGCTTAG GTTTACTCTC AAATGTGAAC 960
CGAAATGCCA CGGTGGAAAT GACCAGGCGT CACATAGGAA GGGGTGTCCG GCTATATTAC 1020
ATCGGTGGAG AGGTGTTTGC AGAGTGCCTA AGTGATAGTG CTATTTTGT TCAGAGTCCA 1080
AACTGTAACC AGCGATATGG ATGGCATCCA GCAACTGTAT GTAAGATTCC TCCAGGATGC 1140
AATCTGAAGA TTTTCAATAA TCAAGAGTTT GCGGCTCTCC TCGCTCAGTC TGTGAATCAA 1200
GGCTTTGAAG CAGTTTATCA GTTAACTCGA ATGTGCACCA TAAGGATGAG CTTTGTAATAA 1260
GGCTGGGGTG CTGAATACAG GCGACAGACC GTTACAAGCA CTCCATGCTG GATTGAGCTT 1320
CACCTGAATG GACCTTTGCA GTGGTTGGAC AAAGTGTGTA CACAGATGGG ATCCCCTTCA 1380
GTCCGCTGCT CAAGCATGTC CTAATGGTCT CCTCTTTTTA ATGTATTACC TGCGGGCGGC 1440
AACTGCAGTC CCAGCAACAG ACTCAATACA GCTTGCTGTG CGTAGTATTT GTGTGTGGTG 1500
CCCATGAATC GTTTACAATC CAAAAGAGAG AGAATAAAAA AGCAAAAACA GCACTTGAGA 1560
TCCCATCAAC GAAAAGCACC TTGTTGGATG ATGTTTCTGA TACTCTTAAA GTAGATCCGT 1620
GTATAAATGA CTCCTTACCT GGGAAAAGGG ACTTTTTT 1658

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 467 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xenopus Smad2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	Met	Ser	Ser	Ile	Leu	Pro	Phe	Thr	Pro	Pro	Val	Val	Lys	Arg	Leu	Leu
	1				5				10						15	
5	Gly	Trp	Lys	Lys	Ser	Ala	Ser	Gly	Thr	Thr	Gly	Ala	Gly	Gly	Asp	Glu
				20					25					30		
	Gln	Asn	Gly	Gln	Glu	Glu	Lys	Trp	Cys	Glu	Lys	Ala	Val	Lys	Ser	Leu
			35					40					45			
	Val	Lys	Lys	Leu	Lys	Lys	Thr	Gly	Gln	Leu	Asp	Glu	Leu	Glu	Lys	Ala
	50						55					60				
10	Ile	Thr	Thr	Gln	Asn	Cys	Asn	Thr	Lys	Cys	Val	Thr	Ile	Pro	Ser	Thr
	65				70						75				80	
	Cys	Ser	Glu	Ile	Trp	Gly	Leu	Ser	Thr	Ala	Asn	Thr	Ile	Asp	Gln	Trp
				85						90					95	
	Asp	Thr	Thr	Gly	Leu	Tyr	Ser	Phe	Ser	Glu	Gln	Thr	Arg	Ser	Leu	Asp
15				100					105					110		
	Gly	Arg	Leu	Gln	Val	Ser	His	Arg	Lys	Gly	Leu	Pro	His	Val	Ile	Tyr
			115					120						125		
	Cys	Arg	Leu	Trp	Arg	Trp	Pro	Asp	Leu	His	Ser	His	His	Glu	Leu	Lys
	130						135					140				
20	Ala	Ile	Glu	Asn	Cys	Glu	Tyr	Ala	Phe	Asn	Leu	Lys	Lys	Asp	Glu	Val
	145				150					155					160	
	Cys	Val	Asn	Pro	Tyr	His	Tyr	Gln	Arg	Val	Glu	Thr	Pro	Val	Leu	Pro
				165					170						175	
	Pro	Val	Leu	Val	Pro	Arg	His	Thr	Glu	Ile	Leu	Thr	Glu	Leu	Pro	Pro
25				180					185					190		
	Leu	Asp	Asp	Tyr	Thr	His	Ser	Ile	Pro	Glu	Asn	Thr	Asn	Phe	Pro	Ala
			195					200					205			
	Gly	Ile	Glu	Pro	Gln	Ser	Asn	Tyr	Ile	Pro	Glu	Thr	Pro	Pro	Pro	Gly
	210					215					220					
30	Tyr	Ile	Ser	Glu	Asp	Gly	Glu	Thr	Ser	Asp	Gln	Gln	Leu	Asn	Gln	Ser
	225				230					235					240	
	Met	Asp	Thr	Gly	Ser	Pro	Ala	Glu	Leu	Ser	Pro	Ser	Thr	Leu	Ser	Pro
				245					250					255		
	Val	Asn	His	Asn	Leu	Asp	Leu	Gln	Pro	Val	Thr	Tyr	Ser	Glu	Pro	Ala
35				260					265					270		
	Phe	Trp	Cys	Ser	Ile	Ala	Tyr	Tyr	Glu	Leu	Asn	Gln	Arg	Val	Gly	Glu
			275				280						285			
	Thr	Phe	His	Ala	Ser	Gln	Pro	Ser	Leu	Thr	Val	Asp	Gly	Phe	Thr	Asp
	290					295						300				
40	Pro	Ser	Asn	Ser	Glu	Arg	Phe	Cys	Leu	Gly	Leu	Leu	Ser	Asn	Val	Asn
	305				310						315				320	
	Arg	Asn	Ala	Thr	Val	Glu	Met	Thr	Arg	Arg	His	Ile	Gly	Arg	Gly	Val
				325					330					335		
	Arg	Leu	Tyr	Tyr	Ile	Gly	Gly	Glu	Val	Phe	Ala	Glu	Cys	Leu	Ser	Asp
45				340					345					350		
	Ser	Ala	Ile	Phe	Val	Gln	Ser	Pro	Asn	Cys	Asn	Gln	Arg	Tyr	Gly	Trp
			355					360					365			
	His	Pro	Ala	Thr	Val	Cys	Lys	Ile	Pro	Pro	Gly	Cys	Asn	Leu	Lys	Ile
	370					375						380				
50	Phe	Asn	Asn	Gln	Glu	Phe	Ala	Ala	Leu	Leu	Ala	Gln	Ser	Val	Asn	Gln
	385				390						395				400	
	Gly	Phe	Glu	Ala	Val	Tyr	Gln	Leu	Thr	Arg	Met	Cys	Thr	Ile	Arg	Met
				405					410					415		

Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr
420 425 430
Ser Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp
435 440 445
5 Leu Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser
450 455 460
Ser Met Ser
465

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xenopus Smad2 MH2 domain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Trp Cys Ser Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu Thr
1 5 10 15
Phe His Ala Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp Pro
20 25 30
Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn Arg
35 40 45
Asn Ala Thr Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val Arg
50 55 60
Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp Ser
65 70 75 80
Ala Ile Phe Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp His
85 90 95
Pro Ala Thr Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile Phe
100 105 110
Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln Gly
115 120 125
Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met Ser
130 135 140
Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr Ser
145 150 155 160
Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp Leu
165 170 175
Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser Ser
180 185 190
Met Ser

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1401 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Human Smad2 coding region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGTCGTCCA TCTTGCCATT CACGCCGCCA GTTGTGAAGA GACTGCTGGG ATGGAAGAAG 60
TCAGCTGGTG GGTCTGGAGG AGCAGGCCGA GGAGAGCAGA ATGGGCAGGA AGAAAAGTGG 120
TGTGAGAAAG CAGTGAAAAG TCTGGTGAAG AAGCTAAAGA AAACAGGACG ATTAGATGAG 180
CTTGAGAAAG CCATCACCAC TCAAACTGT AATACTAAAT GTGTTACCAT ACCAAGCACT 240
TGCTCTGAAA TTTGGGGACT GAGTACACCA AATACGATAG ATCAGTGGGA TACAACAGGC 300
CTTTACAGCT TCTCTGAACA AACCAAGTCT CTTGATGGTC GTCTCCAGGT ATCCCATCGA 360
AAAGGATTGC CACATGTTAT ATATTGCCGA TTATGGCGCT GGCCTGATCT TCACAGTCAT 420
CATGAACTCA AGGCAATTGA AACTGCGAA TATGCTTTTA ATCTTAAAAA GGATGAAGTA 480
TGTGTAAACC CTTACCACTA TCAGAGAGTT GAGACACCAG TTTTGCCTCC AGTATTAGTG 540
CCCCGACACA CCGAGATCCT AACAGAACTT CCGCCTCTGG ATGACTATAC TCACTCCATT 600
CCAGAAAACA CTAACCTCCC AGCAGGAATT GAGCCACAGA GTAATTATAT TCCAGAAACG 660
CCACCTCTG GATATATCAG TGAAGATGGA GAAACAAGTG ACCAACAGTT GAATCAAAGT 720
ATGGACACAG GCTCTCCAGC AGAATATCT CCTACTACTC TTTCCCCTGT TAATCATAGC 780
TTGGATTAC AGCCAGTTAC TTACTCAGAA CCTGCATTTT GGTGTTCAAT AGCATATTAT 840
GAATTAAATC AGAGGGTTGG AGAAACCTTC CATGCATCAC AGCCCTCACT CACTGTAGAT 900
GGCTTTACAG ACCCATCAAA TTCAGAGAGG TTCTGCTTAG GTTTACTCTC CAATGTTAAC 960
CGAAATGCCA CGGTAGAAAT GACAAGAAGG CATATAGGAA GAGGAGTGCG CTTATACTAC 1020
ATAGGTGGGG AAGTTTTTGC TGAGTGCCTA AGTGATAGTG CAATCTTTGT GCAGAGCCCC 1080
AATTGTAATC AGAGATATGG CTGGCACCTT GCAACAGTGT GTAAAATTCC ACCAGGCTGT 1140
AATCTGAAGA TCTTCAACAA CCAGGAATTT GCTGCTCTTC TGGCTCAGTC TGTTAATCAG 1200
GGTTTTGAAG CCGTCTATCA GCTAACTAGA ATGTGCACCA TAAGAATGAG TTTTGTGAAA 1260
GGGTGGGGAG CAGAATACCG AAGGCAGACG GTAACAAGTA CTCCTTGCTG GATTGAACTT 1320
CATCTGAATG GACCTCTACA GTGGTTGGAC AAAGTATTAA CTCAGATGGG ATCCCCTTCA 1380
GTGCGTTGCT CAAGCATGTC A 1401

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Human Smad2

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

	Met	Ser	Ser	Ile	Leu	Pro	Phe	Thr	Pro	Pro	Val	Val	Lys	Arg	Leu	Leu
	1				5					10					15	
	Gly	Trp	Lys	Lys	Ser	Ala	Gly	Gly	Ser	Gly	Gly	Ala	Gly	Gly	Gly	Glu
			20						25					30		
10	Gln	Asn	Gly	Gln	Glu	Glu	Lys	Trp	Cys	Glu	Lys	Ala	Val	Lys	Ser	Leu
		35					40						45			
	Val	Lys	Lys	Leu	Lys	Lys	Thr	Gly	Arg	Leu	Asp	Glu	Leu	Glu	Lys	Ala
	50					55					60					
	Ile	Thr	Thr	Gln	Asn	Cys	Asn	Thr	Lys	Cys	Val	Thr	Ile	Pro	Ser	Thr
15	65				70					75				80		
	Cys	Ser	Glu	Ile	Trp	Gly	Leu	Ser	Thr	Pro	Asn	Thr	Ile	Asp	Gln	Trp
				85					90					95		
	Asp	Thr	Thr	Gly	Leu	Tyr	Ser	Phe	Ser	Glu	Gln	Thr	Arg	Ser	Leu	Asp
				100					105					110		
20	Gly	Arg	Leu	Gln	Val	Ser	His	Arg	Lys	Gly	Leu	Pro	His	Val	Ile	Tyr
		115					120						125			
	Cys	Arg	Leu	Trp	Arg	Trp	Pro	Asp	Leu	His	Ser	His	His	Glu	Leu	Lys
		130					135					140				
25	Ala	Ile	Glu	Asn	Cys	Glu	Tyr	Ala	Phe	Asn	Leu	Lys	Lys	Asp	Glu	Val
	145				150					155				160		
	Cys	Val	Asn	Pro	Tyr	His	Tyr	Gln	Arg	Val	Glu	Thr	Pro	Val	Leu	Pro
				165					170					175		
	Pro	Val	Leu	Val	Pro	Arg	His	Thr	Glu	Ile	Leu	Thr	Glu	Leu	Pro	Pro
			180						185				190			
30	Leu	Asp	Asp	Tyr	Thr	His	Ser	Ile	Pro	Glu	Asn	Thr	Asn	Phe	Pro	Ala
		195					200						205			
	Gly	Ile	Glu	Pro	Gln	Ser	Asn	Tyr	Ile	Pro	Glu	Thr	Pro	Pro	Pro	Gly
		210					215					220				
35	Tyr	Ile	Ser	Glu	Asp	Gly	Glu	Thr	Ser	Asp	Gln	Gln	Leu	Asn	Gln	Ser
	225				230					235				240		
	Met	Asp	Thr	Gly	Ser	Pro	Ala	Glu	Leu	Ser	Pro	Thr	Thr	Leu	Ser	Pro
				245					250					255		
	Val	Asn	His	Ser	Leu	Asp	Leu	Gln	Pro	Val	Thr	Tyr	Ser	Glu	Pro	Ala
			260						265					270		
40	Phe	Trp	Cys	Ser	Ile	Ala	Tyr	Tyr	Glu	Leu	Asn	Gln	Arg	Val	Gly	Glu
		275					280						285			
	Thr	Phe	His	Ala	Ser	Gln	Pro	Ser	Leu	Thr	Val	Asp	Gly	Phe	Thr	Asp
		290					295					300				
45	Pro	Ser	Asn	Ser	Glu	Arg	Phe	Cys	Leu	Gly	Leu	Leu	Ser	Asn	Val	Asn
	305				310					315				320		
	Arg	Asn	Ala	Thr	Val	Glu	Met	Thr	Arg	Arg	His	Ile	Gly	Arg	Gly	Val
				325					330					335		
	Arg	Leu	Tyr	Tyr	Ile	Gly	Gly	Glu	Val	Phe	Ala	Glu	Cys	Leu	Ser	Asp
			340					345					350			
50	Ser	Ala	Ile	Phe	Val	Gln	Ser	Pro	Asn	Cys	Asn	Gln	Arg	Tyr	Gly	Trp
		355					360					365				
	His	Pro	Ala	Thr	Val	Cys	Lys	Ile	Pro	Pro	Gly	Cys	Asn	Leu	Lys	Ile

370 375 380
 Phe Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln
 385 390 395 400
 Gly Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met
 405 410 415
 Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr
 420 425 430
 Ser Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp
 435 440 445
 Leu Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser
 450 455 460
 Ser Met Ser
 465

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Human Smad2 MH2 domain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Trp Cys Ser Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu Thr
 1 5 10 15
 Phe His Ala Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp Pro
 20 25 30
 Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn Arg
 35 40 45
 Asn Ala Thr Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val Arg
 50 55 60
 Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp Ser
 65 70 75 80
 Ala Ile Phe Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp His
 85 90 95
 Pro Ala Thr Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile Phe
 100 105 110
 Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln Gly
 115 120 125
 Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met Ser
 130 135 140
 Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr Ser
 145 150 155 160
 Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp Leu
 165 170 175

Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser Ser
 180 185 190
 Met Ser

5 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...1272
 (D) OTHER INFORMATION:

- (A) NAME/KEY: Other
 (B) LOCATION: 1...1
 (D) OTHER INFORMATION: Human Smad3 coding region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG TCG TCC ATC CTG CCT TTC ACT CCC CCG ATC GTG AAG CGC CTG CTG	48
Met Ser Ser Ile Leu Pro Phe Thr Pro Pro Ile Val Lys Arg Leu Leu	
1 5 10 15	
GGC TGG AAG AAG GGC GAG CAG AAC GGG CAG GAG GAG AAA TGG TGC GAG	96
Gly Trp Lys Lys Gly Glu Gln Asn Gly Gln Glu Glu Lys Trp Cys Glu	
20 25 30	
AAG GCG GTC AAG AGC CTG GTC AAG AAA CTC AAG AAG ACG GGG CAG CTG	144
Lys Ala Val Lys Ser Leu Val Lys Lys Leu Lys Lys Thr Gly Gln Leu	
35 40 45	
GAC GAG CTG GAG AAG GCC ATC ACC ACG CAG AAC GTC AAC ACC AAG TGC	192
Asp Glu Leu Glu Lys Ala Ile Thr Thr Gln Asn Val Asn Thr Lys Cys	
50 55 60	
ATC ACC ATC CCC AGG TCC CTG GAT GGC CGG TTG CAG GTG TCC CAT CGG	240
Ile Thr Ile Pro Arg Ser Leu Asp Gly Arg Leu Gln Val Ser His Arg	
65 70 75 80	
AAG GGG CTC CCT CAT GTC ATC TAC TGC CCT GTG CCA TGG CCA GAC CTG	288
Lys Gly Leu Pro His Val Ile Tyr Cys Pro Val Arg Trp Pro Asp Leu	
85 90 95	
CAC AGC CAC CAC GAG CTG CGG GCC ATG GAG CTG TGT GAG TTC GCC TTC	336
His Ser His His Glu Leu Arg Ala Met Glu Leu Cys Glu Phe Ala Phe	

	100	105	110	
	AAT ATG AAG AAG GAC GAG GTC TGC GTG AAT CCC TAC CAC TAC CAG AGA Asn Met Lys Lys Asp Glu Val Cys Val Asn Pro Tyr His Tyr Gln Arg 115 120 125	384		
5	GTA GAG ACA CCA GTT CTA CCT CCT GTG TTG GTG CCA CGC CAC ACA GAG Val Glu Thr Pro Val Leu Pro Pro Val Leu Val Pro Arg His Thr Glu 130 135 140	432		
10	ATC CCG GCC GAG TTC CCC CCA CTG GAC GAC TAC AGC CAT TCC ATC CCC Ile Pro Ala Glu Phe Pro Pro Leu Asp Asp Tyr Ser His Ser Ile Pro 145 150 155 160	480		
	GAA AAC ACT AAC TTC CCC GCA GGC ATC GAG CCC CAG AGC AAT ATT CCA Glu Asn Thr Asn Phe Pro Ala Gly Ile Glu Pro Gln Ser Asn Ile Pro 165 170 175	528		
15	GAG ACC CCA CCC CCT GGC TAC CTG AGT GAA GAT GGA GAA ACC AGT GAC Glu Thr Pro Pro Pro Gly Tyr Leu Ser Glu Asp Gly Glu Thr Ser Asp 180 185 190	576		
	CAC CAG ATG AAC CAC AGC ATG GAC GCA GGT TCT CCA AAC CTA TCC CCG His Gln Met Asn His Ser Met Asp Ala Gly Ser Pro Asn Leu Ser Pro 195 200 205	624		
20	AAT CCG ATG TCC CCA GCA CAT AAT AAC TTG GAC CTG CAG CCA GTT ACC Asn Pro Met Ser Pro Ala His Asn Asn Leu Asp Leu Gln Pro Val Thr 210 215 220	672		
25	TAC TGC GAG CCG GCC TTC TGG TGC TCC ATC TCC TAC TAC GAG CTG AAC Tyr Cys Glu Pro Ala Phe Trp Cys Ser Ile Ser Tyr Tyr Glu Leu Asn 225 230 235 240	720		
	CAG CGC GTC GGG GAG ACA TTC CAC GCC TCG CAG CCA TCC ATG ACT GTG Gln Arg Val Gly Glu Thr Phe His Ala Ser Gln Pro Ser Met Thr Val 245 250 255	768		
30	GAT GGC TTC ACC GAC CCC TCC AAT TCG GAG CGC TTC TGC CTA GGG CTG Asp Gly Phe Thr Asp Pro Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu 260 265 270	816		
	CTC TCC AAT GTC AAC AGG AAT GCA GCA GTG GAG CTG ACA CGG AGA CAC Leu Ser Asn Val Asn Arg Asn Ala Ala Val Glu Leu Thr Arg Arg His 275 280 285	864		
35	ATC GGA AGA GGC GTG CGG CTC TAC TAC ATC GGA GGG GAG GTC TTC GCA Ile Gly Arg Gly Val Arg Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala 290 295 300	912		
40	GAG TGC CTC AGT GAC AGC GCT ATT TTT GTC CAG TCT CCC AAC TGT AAC Glu Cys Leu Ser Asp Ser Ala Ile Phe Val Gln Ser Pro Asn Cys Asn 305 310 315 320	960		

	CAG CGC TAT GGC TGG CAC CCG GCC ACC GTC TGC AAG ATC CCA CCA GGA	1008
	Gln Arg Tyr Gly Trp His Pro Ala Thr Val Cys Lys Ile Pro Pro Gly	
	325 330 335	
5	TGC AAC CTG AAG ATC TTC AAC AAC CAG GAG TTC GCT GCC CTC CTG GCC	1056
	Cys Asn Leu Lys Ile Phe Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala	
	340 345 350	
	CAG TCG GTC AAC CAG GGC TTT GAG GCT GTC TAC CAG TTG ACC CGA ATG	1104
	Gln Ser Val Asn Gln Gly Phe Glu Ala Val Tyr Gln Leu Thr Arg Met	
	355 360 365	
10	TGC ACC ATC CGC ATG AGC TTC GTC AAA GGC TGG GGA GCG GAG TAC AGG	1152
	Cys Thr Ile Arg Met Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg	
	370 375 380	
	AGA CAG ACT GTG ACC AGT ACC CCC TGC TGG ATT GAG CTG CAC CTG AAT	1200
	Arg Gln Thr Val Thr Ser Thr Pro Cys Trp Ile Glu Leu His Leu Asn	
	385 390 395 400	
	GGG CCT TTG CAG TGG CTT GAC AAG GTC CTC ACC CAG ATG GGC TCC CCA	1248
	Gly Pro Leu Gln Trp Leu Asp Lys Val Leu Thr Gln Met Gly Ser Pro	
	405 410 415	
	AGC ATC CGC TGT TCC AGT GTG TCT TAGAGACATC AAGTATGGTA GGGGAGGGCA	1302
	Ser Ile Arg Cys Ser Ser Val Ser	
	420	
	GGCTTGGGGA AAATGGCCAT ACAGGAGGTG GAGAAAATTG GAACTCTACT CAACCCATTG	1362
	TTGTCAAGGA AGAAGAAATC TTTCTCCCTC AACTGAAGGG GTGCACCCAC CTGTTTTCTG	1422
	AAACACACGA GCAAACCCAG AGGTGGATGT TATGAACAGC TGTGTCTGCC AAACACATTT	1482
	ACCTTTTGGC CCCACTTTGA AGGGCAAGAA ATGGCGTCTG CTCTGGTGGC TTAAGTGAGC	1542
	AGAACAGGTA GTATTACACC ACCGGCACCC TCCCCCAGA CTCTTTTTTT GAGTGACAGC	1602
	TTTCTGGGAT GTCACAGTCC AACCAGAAAG GCCCCTCTGT CTAGGACTGC AGTGTGGAGT	1662
	TCACCTTGGA AGGGCGTTCT AGGTAGGAAG AGCCCGCACG ATGCAGACCT CATGCCCAGC	1722
	TCTCTGACGC TTGTGACAGT GCCTCTTCCA GTGAACATTG CCAGCCCAGC CCCGCCCCGT	1782
	TGTGAGCTGG ATAGACTTGG GATGGGGAGG GAGGGAGTTT TGTCTGTCTC CCTCCCCCTC	1842
	CAGAACATAC TGATTGGGAG GTGCGTGTTC AGCAGAACCT GCACACAGGA CAGCGGGAAA	1902
	AATCGATGAG CGCCACCTCT TTAAAACTC ACTTACGTTG TCCTTTTTCA CTTTGAAAAG	1962
	TTGGAAGGAC TGCTGAGGCC CAGTGCATAT GCAATGTATA GTGTCTATTA TCACATTAAT	2022
	CTCAAAGAGA TTCGAATGAC GGTAAGTGT CTCTGAAGC AGGAGGCCCT TGTCGTGGGA	2082
	TGGCATTGTTG TCTCAGGCAG CACCACACTG GGTGCGTCTC CAGTCATCTG TAAGAGCTTG	2142
	CTCCAGATTG TGATGCATAC GGCTATATTG GTTTATGTAG TCAGTTGCAT TCATTAAATC	2202
	AACTTTATCA TATGCTCAAA AAAAAAAAAA AG	2234

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Human Smad3

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ser Ser Ile Leu Pro Phe Thr Pro Pro Ile Val Lys Arg Leu Leu
1 5 10 15
Gly Trp Lys Lys Gly Glu Gln Asn Gly Gln Glu Glu Lys Trp Cys Glu
20 25 30
Lys Ala Val Lys Ser Leu Val Lys Lys Leu Lys Lys Thr Gly Gln Leu
35 40 45
Asp Glu Leu Glu Lys Ala Ile Thr Thr Gln Asn Val Asn Thr Lys Cys
50 55 60
Ile Thr Ile Pro Arg Ser Leu Asp Gly Arg Leu Gln Val Ser His Arg
65 70 75 80
Lys Gly Leu Pro His Val Ile Tyr Cys Pro Val Arg Trp Pro Asp Leu
85 90 95
His Ser His His Glu Leu Arg Ala Met Glu Leu Cys Glu Phe Ala Phe
100 105 110
Asn Met Lys Lys Asp Glu Val Cys Val Asn Pro Tyr His Tyr Gln Arg
115 120 125
Val Glu Thr Pro Val Leu Pro Pro Val Leu Val Pro Arg His Thr Glu
130 135 140
Ile Pro Ala Glu Phe Pro Pro Leu Asp Asp Tyr Ser His Ser Ile Pro
145 150 155 160
Glu Asn Thr Asn Phe Pro Ala Gly Ile Glu Pro Gln Ser Asn Ile Pro
165 170 175
Glu Thr Pro Pro Pro Gly Tyr Leu Ser Glu Asp Gly Glu Thr Ser Asp
180 185 190
His Gln Met Asn His Ser Met Asp Ala Gly Ser Pro Asn Leu Ser Pro
195 200 205
Asn Pro Met Ser Pro Ala His Asn Asn Leu Asp Leu Gln Pro Val Thr
210 215 220
Tyr Cys Glu Pro Ala Phe Trp Cys Ser Ile Ser Tyr Tyr Glu Leu Asn
225 230 235 240
Gln Arg Val Gly Glu Thr Phe His Ala Ser Gln Pro Ser Met Thr Val
245 250 255
Asp Gly Phe Thr Asp Pro Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu
260 265 270
Leu Ser Asn Val Asn Arg Asn Ala Val Glu Leu Thr Arg Arg His
275 280 285
Ile Gly Arg Gly Val Arg Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala
290 295 300
Glu Cys Leu Ser Asp Ser Ala Ile Phe Val Gln Ser Pro Asn Cys Asn
305 310 315 320
Gln Arg Tyr Gly Trp His Pro Ala Thr Val Cys Lys Ile Pro Pro Gly
325 330 335
Cys Asn Leu Lys Ile Phe Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala
340 345 350
Gln Ser Val Asn Gln Gly Phe Glu Ala Val Tyr Gln Leu Thr Arg Met

355 360 365
 Cys Thr Ile Arg Met Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg
 370 375 380
 Arg Gln Thr Val Thr Ser Thr Pro Cys Trp Ile Glu Leu His Leu Asn
 385 390 395 400
 Gly Pro Leu Gln Trp Leu Asp Lys Val Leu Thr Gln Met Gly Ser Pro
 405 410 415
 Ser Ile Arg Cys Ser Ser Val Ser
 420

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Human Smad3 MH2 domain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Trp Cys Ser Ile Ser Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu Thr
 1 5 10 15
 Phe His Ala Ser Gln Pro Ser Met Thr Val Asp Gly Phe Thr Asp Pro
 20 25 30
 Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn Arg
 35 40 45
 Asn Ala Ala Val Glu Leu Thr Arg Arg His Ile Gly Arg Gly Val Arg
 50 55 60
 Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp Ser
 65 70 75 80
 Ala Ile Phe Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp His
 85 90 95
 Pro Ala Thr Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile Phe
 100 105 110
 Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln Gly
 115 120 125
 Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met Ser
 130 135 140
 Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr Ser
 145 150 155 160
 Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp Leu
 165 170 175
 Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Ile Arg Cys Ser Ser
 180 185 190
 Val Ser

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1605 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...1554
(D) OTHER INFORMATION:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Xenopus FAST-1 coding region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG AGA GAC CCC TCC AGT CTG TAC TCA GGA TTC CCA GCT GGA TCC CAG	48
Met Arg Asp Pro Ser Ser Leu Tyr Ser Gly Phe Pro Ala Gly Ser Gln	
1 5 10 15	
TAT GAA AGT GTG GAG CCT CCC AGC CTT GCC CTG CTG AGC TCT ATA GAC	96
Tyr Glu Ser Val Glu Pro Pro Ser Leu Ala Leu Leu Ser Ser Ile Asp	
20 25 30	
CAG GAG CAG CTC CCA GTG GCC ACC GGC CAG TCC TAT AAT CAC AGT GTC	144
Gln Glu Gln Leu Pro Val Ala Thr Gly Gln Ser Tyr Asn His Ser Val	
35 40 45	
CAG CCT TGG CCC CAA CCT TGG CCA CCC TTG TCC CTG TAC AGA GAG GGG	192
Gln Pro Trp Pro Gln Pro Trp Pro Pro Leu Ser Leu Tyr Arg Glu Gly	
50 55 60	
GGC ACG TGG AGC CCA GAC AGA GGC AGT ATG TAT GGA CTC TCC CCC GGC	240
Gly Thr Trp Ser Pro Asp Arg Gly Ser Met Tyr Gly Leu Ser Pro Gly	
65 70 75 80	
ACC CAC GAG GGC TCC TGC ACC CAC ACT CAC GAG GGC CCC AAG GAC TCA	288
Thr His Glu Gly Ser Cys Thr His Thr His Glu Gly Pro Lys Asp Ser	
85 90 95	
ATG GCA GGA GAC CAG ACC AGG TCC AGG AAG AGC AAA AAG AAG AAT TAT	336
Met Ala Gly Asp Gln Thr Arg Ser Arg Lys Ser Lys Lys Lys Asn Tyr	
100 105 110	
CAT CGA TAT AAC AAG CCC CCC TAT TCC TAC CTG GCT ATG ATT GCC CTG	384
His Arg Tyr Asn Lys Pro Pro Tyr Ser Tyr Leu Ala Met Ile Ala Leu	
115 120 125	

		GTC ATC CAG AAC TCG CCC GAG AAG AGG CTC AAA CTC TCC CAG ATC CTG	432
		Val Ile Gln Asn Ser Pro Glu Lys Arg Leu Lys Leu Ser Gln Ile Leu	
		130 135 140	
5		AAG GAG GTC AGT ACA CTC TTC CCC TTC TTT AAT GGG GAT TAT ATG GGT	480
		Lys Glu Val Ser Thr Leu Phe Pro Phe Phe Asn Gly Asp Tyr Met Gly	
		145 150 155 160	
		TGG AAA GAC TCC ATC AGG CAC AAC TTG TCT TCC AGT GAC TGC TTT AAG	528
		Trp Lys Asp Ser Ile Arg His Asn Leu Ser Ser Ser Asp Cys Phe Lys	
		165 170 175	
10		AAG ATT CTC AAA GAC CCT GGA AAG CCC CAG GCC AAG GGT AAC TTC TGG	576
		Lys Ile Leu Lys Asp Pro Gly Lys Pro Gln Ala Lys Gly Asn Phe Trp	
		180 185 190	
		ACG GTG GAT GTT AGC CGG ATT CCT CTG GAT GCG ATG AAG CTG CAG AAC	624
		Thr Val Asp Val Ser Arg Ile Pro Leu Asp Ala Met Lys Leu Gln Asn	
15		195 200 205	
		ACT GCG TTG ACC CGA GGT GGA TCA GAC TAC TTT GTC CAG GAT TTG GCT	672
		Thr Ala Leu Thr Arg Gly Gly Ser Asp Tyr Phe Val Gln Asp Leu Ala	
		210 215 220	
20		CCA TAC ATC CTA CAT AAC TAT AAA TAT GAG CAC AAT GCA GGG GCG TAT	720
		Pro Tyr Ile Leu His Asn Tyr Lys Tyr Glu His Asn Ala Gly Ala Tyr	
		225 230 235 240	
		GGT CAC CAG ATG CCT CCA AGT CAT GCC AGA TCC CTG TCT TTG GCA GAG	768
		Gly His Gln Met Pro Pro Ser His Ala Arg Ser Leu Ser Leu Ala Glu	
		245 250 255	
25		GAC TCT CAA CAG ACC AAC ACT GGT GGC AAA CTT AAC ACA TCC TTT ATG	816
		Asp Ser Gln Gln Thr Asn Thr Gly Gly Lys Leu Asn Thr Ser Phe Met	
		260 265 270	
		ATT GAT TCC CTA CTC CAT GAC CTG CAA GAG GTG GAT CTG CCT GAT GCC	864
		Ile Asp Ser Leu Leu His Asp Leu Gln Glu Val Asp Leu Pro Asp Ala	
30		275 280 285	
		TCC AGG AAC CTT GAG AAC CAA AGG ATC TCT CCG GCT GTA GCC ATG AAC	912
		Ser Arg Asn Leu Glu Asn Gln Arg Ile Ser Pro Ala Val Ala Met Asn	
		290 295 300	
35		AAT ATG TGG AGC TCT GCT CCT CTT CTC TAC ACT CAT TCC AAG CCA ACA	960
		Asn Met Trp Ser Ser Ala Pro Leu Leu Tyr Thr His Ser Lys Pro Thr	
		305 310 315 320	
		AGG AAT GCC AGA AGC CCT GGT TTG TCC ACC ATC CAT TCC ACG TAC TCC	1008
		Arg Asn Ala Arg Ser Pro Gly Leu Ser Thr Ile His Ser Thr Tyr Ser	
		325 330 335	
40		TCT TCC AGC TCC AGC ATT TCT ACA ATC TCC CCC GTT GGG TTT CAG AAG	1056
		Ser Ser Ser Ser Ser Ile Ser Thr Ile Ser Pro Val Gly Phe Gln Lys	

[illegible]

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 534 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xenopus FAST-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Arg Asp Pro Ser Ser Leu Tyr Ser Gly Phe Pro Ala Gly Ser Gln
1 5 10 15
Tyr Glu Ser Val Glu Pro Pro Ser Leu Ala Leu Leu Ser Ser Ile Asp
20 25 30
Gln Glu Gln Leu Pro Val Ala Thr Gly Gln Ser Tyr Asn His Ser Val
35 40 45
Gln Pro Trp Pro Gln Pro Trp Pro Pro Leu Ser Leu Tyr Arg Glu Gly
50 55 60
Gly Thr Trp Ser Pro Asp Arg Gly Ser Met Tyr Gly Leu Ser Pro Gly
65 70 75 80
Thr His Glu Gly Ser Cys Thr His Thr His Glu Gly Pro Lys Asp Ser
85 90 95
Met Ala Gly Asp Gln Thr Arg Ser Arg Lys Ser Lys Lys Asn Tyr
100 105 110
His Arg Tyr Asn Lys Pro Pro Tyr Ser Tyr Leu Ala Met Ile Ala Leu
115 120 125
Val Ile Gln Asn Ser Pro Glu Lys Arg Leu Lys Leu Ser Gln Ile Leu
130 135 140
Lys Glu Val Ser Thr Leu Phe Pro Phe Phe Asn Gly Asp Tyr Met Gly
145 150 155 160
Trp Lys Asp Ser Ile Arg His Asn Leu Ser Ser Ser Asp Cys Phe Lys
165 170 175
Lys Ile Leu Lys Asp Pro Gly Lys Pro Gln Ala Lys Gly Asn Phe Trp
180 185 190
Thr Val Asp Val Ser Arg Ile Pro Leu Asp Ala Met Lys Leu Gln Asn
195 200 205
Thr Ala Leu Thr Arg Gly Gly Ser Asp Tyr Phe Val Gln Asp Leu Ala
210 215 220
Pro Tyr Ile Leu His Asn Tyr Lys Tyr Glu His Asn Ala Gly Ala Tyr
225 230 235 240
Gly His Gln Met Pro Pro Ser His Ala Arg Ser Leu Ser Leu Ala Glu
245 250 255
Asp Ser Gln Gln Thr Asn Thr Gly Gly Lys Leu Asn Thr Ser Phe Met
260 265 270
Ile Asp Ser Leu Leu His Asp Leu Gln Glu Val Asp Leu Pro Asp Ala
275 280 285
Ser Arg Asn Leu Glu Asn Gln Arg Ile Ser Pro Ala Val Ala Met Asn
290 295 300
Asn Met Trp Ser Ser Ala Pro Leu Leu Tyr Thr His Ser Lys Pro Thr
305 310 315 320
Arg Asn Ala Arg Ser Pro Gly Leu Ser Thr Ile His Ser Thr Tyr Ser
325 330 335

Ser Ser Ser Ser Ser Ile Ser Thr Ile Ser Pro Val Gly Phe Gln Lys
340 345 350
Glu Gln Glu Lys Ser Gly Arg Gln Thr Gln Arg Val Gly His Pro Ile
355 360 365
5 Lys Arg Ser Arg Glu Asp Asp Asp Cys Ser Thr Thr Ser Ser Asp Pro
370 375 380
Asp Thr Gly Asn Tyr Ser Pro Ile Glu Pro Pro Lys Lys Met Pro Leu
385 390 395 400
10 Leu Ser Leu Asp Leu Pro Thr Ser Tyr Thr Lys Ser Val Ala Pro Asn
405 410 415
Val Val Ala Pro Pro Ser Val Leu Pro Phe Phe His Phe Pro Arg Phe
420 425 430
Thr Tyr Tyr Asn Tyr Gly Pro Ser Pro Tyr Met Thr Pro Pro Tyr Trp
435 440 445
15 Gly Phe Pro His Pro Thr Asn Ser Gly Gly Asp Ser Pro Arg Gly Pro
450 455 460
Gln Ser Pro Leu Asp Leu Asp Asn Met Leu Arg Ala Met Pro Pro Asn
465 470 475 480
20 Lys Ser Val Phe Asp Val Leu Thr Ser His Pro Gly Asp Leu Val His
485 490 495
Pro Ser Phe Leu Ser Gln Cys Leu Gly Ser Ser Gly Ser Pro Tyr Pro
500 505 510
Ser Arg Gln Gly Leu Met Tyr Arg Arg Arg Pro Pro Gly Leu Thr Trp
515 520 525
25 Ser Gly His Ser Met Lys
530

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xenopus FAST-1 SID

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Thr Ser Ser Asp Pro Asp Thr Gly Asn Tyr Ser Pro Ile Glu Pro Pro
1 5 10 15
Lys Lys Met Pro Leu Leu Ser Leu Asp Leu Pro Thr Ser Tyr Thr Lys
20 25 30
Ser Val Ala Pro Asn Val Val Ala Pro Pro Ser Val Leu Pro Phe Phe
35 40 45
45 His Phe Pro Arg Phe Thr Tyr Tyr Asn Tyr Gly Pro Ser Pro Tyr Met
50 55 60
Thr Pro Pro Tyr Trp Gly Phe Pro His Pro Thr Asn Ser Gly Gly Asp
65 70 75 80

Ser Pro Arg Gly Pro Gln Ser Pro Leu Asp Leu Asp Asn Met Leu Arg
85 90 95
Ala Met Pro Pro Asn Lys Ser Val Phe Asp Val Leu Thr Ser His Pro
100 105 110
5 Gly Asp Leu Val His Pro Ser Phe Leu Ser Gln Cys Leu Gly Ser Ser
115 120 125
Gly Ser Pro Tyr Pro Ser Arg Gln Gly Leu Met Tyr Arg Arg Arg Pro
130 135 140
10 Pro Gly Leu Thr Trp Ser Gly His Ser Met Lys
145 150 155

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1634 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Human FAST-1 coding region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATGGGGCCCT GCAGCGGCTC CCGCCTGGGG CCCCCAGAGG CTGAGTCGCC CTCCCAGCCC 60
CCTAAGAGGA GGAAGAAGAG GTACCTGCGA CATGACAAGC CCCCTACAC CTACTTGGCC 120
ATGATCGCCT TGGTGATTCA GGCCGCTCCC TCCCGCAGAC TGAAGCTGGC CCAGATCATC 180
CGTCAGGTCC AGGCCGTGTT CCCCTTCTTC AGGGAAGACT ACGAGGGCTG GAAAGACTCC 240
ATTCGCCACA ACCTTTCCTC CAACCGATGC TTCCGCAAGG TGCCCAAGGA CCCTGCAAAG 300
CCCCAGGCCA AGGGCAACTT CTGGGCGGTC GACGTGAGCC TGATCCAGC TGAGGCGCTC 360
CGGCTGCAGA ACACCGCCCT GTGCCGGCGC TGGCAGAACG GAGGTGCGCG TGGAGCCTTC 420
GCCAAGGACC TGGGCCCCCTA CGTGCTGCAC GGCCGGCCAT ACCGGCCGCC CAGTCCCCCG 480
CCACCACCCA GTGAGGGGCTT CAGCATCAAG TCCCTGCTAA GAAGGTCCGG GGAAGGGGCA 540
CCCTGGCCGG GGCTAGCTCC ACAGAACAGC CCAGTTCCTG CAGGCACAGG GAACAATGGG 600
GAAGAAGCGG TGCCCACCCC ACCCCTTCCC TCTTCTGAAA GGCTCTGTG GCCCTCTGC 660
35 CCCCTTCCTG GCCCCACGAG AGTGGAGGGG GAGACTGTGC AGGGGGGAGC CATGGGCCCT 720
CAACCCTCTC CCCAGAGCCT AGGGCCTGGC CTTTCCACTA CTGCAGGGCA CCGCAGTTCT 780
GGGGGACGGT CCAGCGGGGG ACACAGGGCC TCCCTTTGGG GGCAGCTGCC CACCTCCTAC 840
TTGCCTATCT ACACTCCCAA TGTGGTAATG CCCTTGGCAC CACCACCCAC CTCCTGTCCC 900
CAGTGTCGGT CAACCAGCCC TGCCTACTGG GGGGTGGCCC CTGAAACCCG AGGGCCCCCA 960
40 GGGCTGCTCT GCGATCTAAA CGCCTCTTC CAAGGGGTGC CACCAACAA AAGCATCTAC 1020
GACGTTTGGG TCAGCCACCC TCGGGACCTG GCGGCCCTG GCCCAGGCTG GCTGCTCTCC 1080
TGGTGCAGCC TGTGAGGCTC TTAAGACAGG GGCCGCTCCT CCCTCCCGCT CCCACCCCA 1140
CCTTGTTGAC AGGGAGCCAA GGCGAGGCGG CTGTCTGCGA CACAGCAGC CTCGAAACAC 1200
CAGGCAGCAG CCTTGCTGGG AGTCCACGGT GTTTATTGGG CCACCCACG CATGGCCGTG 1260
45 GCCCAGCTGG GCACAACCCT CACCCTGGTC TGTCAATGCT GTTTTTCCTA CACTCAGCGG 1320
CAAACTGCA GGAGCAGGCT GAACCTGAAT ATCCCTTCTT AATCCCTCTT CTCAGCCAC 1380
TACCCATCCA TCAGTCACCA GCCGTCACCT CCTCCCGTG CTCCAGCTGG GGAAGGAAA 1440
ACCCATGTGG ATCACCCTGAA ATCCTGCCCT CTCTCTCTGT CGGAAAAGAA GTCCACCTTT 1500

TTCCGGAAC CGGTTAGGGA ATTAAATGC CCTACATGTC CTGGTGGTTG GGGGGGAAAC 1560
 CACTAAAGGA ATTTGCAACC TTTTATCC TCTTCATTT ATCCCAAGGG GGGGCCCGTC 1620
 CCATTTCCCC AACC 1634

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Human FAST-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Gly	Pro	Cys	Ser	Gly	Ser	Arg	Leu	Gly	Pro	Pro	Glu	Ala	Glu	Ser	1	5	10	15
Pro	Ser	Gln	Pro	Pro	Lys	Arg	Arg	Lys	Lys	Arg	Tyr	Leu	Arg	His	Asp	20	25	30	
Lys	Pro	Pro	Tyr	Thr	Tyr	Leu	Ala	Met	Ile	Ala	Leu	Val	Ile	Gln	Ala	35	40	45	
Ala	Pro	Ser	Arg	Arg	Leu	Lys	Leu	Ala	Gln	Ile	Ile	Arg	Gln	Val	Gln	50	55	60	
Ala	Val	Phe	Pro	Phe	Phe	Arg	Glu	Asp	Tyr	Glu	Gly	Trp	Lys	Asp	Ser	65	70	75	80
Ile	Arg	His	Asn	Leu	Ser	Ser	Asn	Arg	Cys	Phe	Arg	Lys	Val	Pro	Lys	85	90	95	
Asp	Pro	Ala	Lys	Pro	Gln	Ala	Lys	Gly	Asn	Phe	Trp	Ala	Val	Asp	Val	100	105	110	
Ser	Leu	Ile	Pro	Ala	Glu	Ala	Leu	Arg	Leu	Gln	Asn	Thr	Ala	Leu	Cys	115	120	125	
Arg	Arg	Trp	Gln	Asn	Gly	Gly	Ala	Arg	Gly	Ala	Phe	Ala	Lys	Asp	Leu	130	135	140	
Gly	Pro	Tyr	Val	Leu	His	Gly	Arg	Pro	Tyr	Arg	Pro	Pro	Ser	Pro	Pro	145	150	155	160
Pro	Pro	Pro	Ser	Glu	Gly	Phe	Ser	Ile	Lys	Ser	Leu	Leu	Arg	Arg	Ser	165	170	175	
Gly	Glu	Gly	Ala	Pro	Trp	Pro	Gly	Leu	Ala	Pro	Gln	Asn	Ser	Pro	Val	180	185	190	
Pro	Ala	Gly	Thr	Gly	Asn	Asn	Gly	Glu	Glu	Ala	Val	Pro	Thr	Pro	Pro	195	200	205	
Leu	Pro	Ser	Ser	Glu	Arg	Pro	Leu	Trp	Pro	Leu	Cys	Pro	Leu	Pro	Gly	210	215	220	
Pro	Thr	Arg	Val	Glu	Gly	Glu	Thr	Val	Gln	Gly	Gly	Ala	Met	Gly	Pro	225	230	235	240
Gln	Pro	Ser	Pro	Gln	Ser	Leu	Gly	Pro	Gly	Leu	Ser	Thr	Thr	Ala	Gly	245	250	255	

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His Arg Ser Ser Gly Gly Arg Ser Ser Gly Gly His Arg Ala Ser Leu
      260                      265                      270
Trp Gly Gln Leu Pro Thr Ser Tyr Leu Pro Ile Tyr Thr Pro Asn Val
      275                      280                      285
Val Met Pro Leu Ala Pro Pro Pro Thr Ser Cys Pro Gln Cys Pro Ser
      290                      295                      300
Thr Ser Pro Ala Tyr Trp Gly Val Ala Pro Glu Thr Arg Gly Pro Pro
      305                      310                      315                      320
Gly Leu Leu Cys Asp Leu Asn Ala Leu Phe Gln Gly Val Pro Pro Asn
      325                      330                      335
Lys Ser Ile Tyr Asp Val Trp Val Ser His Pro Arg Asp Leu Ala Ala
      340                      345                      350
Pro Gly Pro Gly Trp Leu Leu Ser Trp Cys Ser Leu Glx Gly Ser Glx
      355                      360                      365
Asp Arg Gly Arg Ser Ser Leu Pro Leu Pro Pro Pro Pro Cys Glx Gln
      370                      375                      380
Gly Ala Lys Ala Arg Arg Leu Ser Ala Thr Thr Ala Ala Ser Lys His
      385                      390                      395                      400
Gln Ala Ala Ala Leu Leu Gly Val His Gly Val Tyr Trp Ala Thr Pro
      405                      410                      415
Arg Met Ala Val Ala Gln Leu Gly Thr Thr Leu Thr Leu Val Cys His
      420                      425                      430
Ala Cys Phe Ser Tyr Thr Gln Arg Gln Asn Cys Arg Ser Arg Leu Asn
      435                      440                      445
Leu Asn Ile Pro Ser Glx Ser Leu Phe Ser Ala His Tyr Pro Ser Ile
      450                      455                      460
Ser His Gln Pro Ser Pro Pro Ser Arg Ala Pro Ala Gly Gly Arg Lys
      465                      470                      475                      480
Thr His Val Asp His Leu Lys Ser Cys Pro Leu Ser Leu Ser Glu Lys
      485                      490                      495
Lys Ser Thr Phe Phe Arg Lys Pro Val Arg Glu Leu Lys Cys Pro Thr
      500                      505                      510
Cys Pro Gly Gly Trp Gly Gly Asn His Glx Arg Asn Leu Gln Pro Phe
      515                      520                      525
Leu Ser Ser Phe Ile Tyr Pro Lys Gly Gly Pro Val Pro Phe Pro Gln
      530                      535                      540

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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Human FAST-1 SID

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

5
10
15
20
25
30
35
40

Gln	Gly	Gly	Ala	Met	Gly	Pro	Gln	Pro	Ser	Pro	Gln	Ser	Leu	Gly	Pro
1				5					10					15	
Gly	Leu	Ser	Thr	Thr	Ala	Gly	His	Arg	Ser	Ser	Gly	Gly	Arg	Ser	Ser
			20					25					30		
Gly	Gly	His	Arg	Ala	Ser	Leu	Trp	Gly	Gln	Leu	Pro	Thr	Ser	Tyr	Leu
		35					40				45				
Pro	Ile	Tyr	Thr	Pro	Asn	Val	Val	Met	Pro	Leu	Ala	Pro	Pro	Pro	Thr
	50					55					60				
Ser	Cys	Pro	Gln	Cys	Pro	Ser	Thr	Ser	Pro	Ala	Tyr	Trp	Gly	Val	Ala
65				70					75					80	
Pro	Glu	Thr	Arg	Gly	Pro	Pro	Gly	Leu	Leu	Cys	Asp	Leu	Asn	Ala	Leu
			85					90					95		
Phe	Gln	Gly	Val	Pro	Pro	Asn	Lys	Ser	Ile	Tyr	Asp	Val	Trp	Val	Ser
			100				105						110		
His	Pro	Arg	Asp	Leu	Ala	Ala	Pro	Gly	Pro	Gly	Trp	Leu	Leu	Ser	Trp
		115					120					125			
Cys	Ser	Leu	Glx	Gly	Ser	Glx	Asp	Arg	Gly	Arg	Ser	Ser	Leu	Pro	Leu
	130					135					140				
Pro	Pro	Pro	Pro	Cys	Glx	Gln	Gly	Ala	Lys	Ala	Arg	Arg	Leu	Ser	Ala
145				150					155					160	
Thr	Thr	Ala	Ala	Ser	Lys	His	Gln	Ala	Ala	Ala	Leu	Leu	Gly	Val	His
			165					170					175		
Gly	Val	Tyr	Trp	Ala	Thr	Pro	Arg	Met	Ala	Val	Ala	Gln	Leu	Gly	Thr
		180					185						190		
Thr	Leu	Thr	Leu	Val	Cys	His	Ala	Cys	Phe	Ser	Tyr	Thr	Gln	Arg	Gln
	195					200					205				
Asn	Cys	Arg	Ser	Arg	Leu	Asn	Leu	Asn	Ile	Pro	Ser	Glx	Ser	Leu	Phe
	210					215					220				
Ser	Ala	His	Tyr	Pro	Ser	Ile	Ser	His	Gln	Pro	Ser	Pro	Pro	Ser	Arg
225				230					235					240	
Ala	Pro	Ala	Gly	Gly	Arg	Lys	Thr	His	Val	Asp	His	Leu	Lys	Ser	Cys
			245					250					255		
Pro	Leu	Ser	Leu	Ser	Glu	Lys	Lys	Ser	Thr	Phe	Phe	Arg	Lys	Pro	Val
		260					265						270		
Arg	Glu	Leu	Lys	Cys	Pro	Thr	Cys	Pro	Gly	Gly	Trp	Gly	Gly	Asn	His
	275						280					285			
Glx	Arg	Asn	Leu	Gln	Pro	Phe	Leu	Ser	Ser	Phe	Ile	Tyr	Pro	Lys	Gly
	290					295					300				
Gly	Pro	Val	Pro	Phe	Pro	Gln									
305					310										

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1668 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1

(D) OTHER INFORMATION: Mouse FAST-1 coding region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

5 ATGGCCTCGG GCTGGGACCT GGCCTCAACT TACACTCCGA CTACCCCGAG CCCCAGTTA 60
GCCCTGGCTC CGGCCAGGG CTACCTCCCT TGTATGGGC CTCGCGACAA CTCTCAGCTG 120
AGGCCTCCAG AGGCAGAGTC TCTTTCGAAG ACCCCCAAGA GGAGGAAGAA GAGATACCTA 180
CGGCATGACA AGCCCCCTA CACCTACTTG GCCATGATCG CCTTGGTAAT TCAGGCCGCA 240
CCCTTCCGCA GGCTGAAACT GGCTCAGGTC CAGGCAGTGT TCCCCTTCTT CAGGGACGAC 300
TATGAGGGTG GGAAGGACTC CATCCGCCAC AACCTTTCCT CTAATCGGTG CTTCCATAAG 360
10 GTGCCCCAAG ACCCTGCAAA GCCCAGGCC AAGGGCAACT TCTGGGCGGT GGATGTTAGC 420
CTGATTCTCTG CTGAGGCGCT GCGCCTTCAG AACACTGCCG TGTGCCGTCG ATGGCAGAAC 480
CGGGGCACCC ACAGAGCTTT CGCCAAGGAC CTGAGCCCTT ACGTGCTCCA CGGCCAGCCT 540
TATCAGCCAC CCAGTCCCCC ACCACCACCT AGGGAGGGTT TCAGCATCAA GTCCCTGCTA 600
GGGGACCCTG GGAAAGAATC CACATGGCCC CAGCATCCTG GGCTCCCTGG ACAGAGCACT 660
15 GCAGCTCAGG CAGGCACCTT GTCAAAGGGG GAAGAAGGGA TGGGCACTGG ACCCTCTAGC 720
TCCTCTGAGA CGCTCTGTG GCCCTCTGCG TCCCTTCTCTG GGCCACAAT CATAGAGGGG 780
GAGAGTTCCC AAGGGGAGGT AATCAGGCCT TCTCCCGTCA CCCCAGATCA AGGCTCCTGG 840
CCCTCCACT TACTTGAGGA TTCCGCAGAT TCCAGGGGAG TGCCAGGAG GGGGAGCAGA 900
GCCTCCTTGT GGGGACAGCT ACCCACTTCT TACTTGCCA TCTATACGCC CAATGTAGTA 960
20 ATGCCCTTGG CCACACTACC GACCACCTCT TGTCCCCAGT GCCCATCTTC TGCCAGCCCA 1020
GCTTACTGGA GCGTAGGCAC TGAATCCCAA GGGTCCCAGG ACCTGCTCTG TGATCTAGAC 1080
TCCCTCTTCC AGGGAGTACC ACCCAACAAG AGTATCTATG ATGTGTGGGT CAGCCATCCT 1140
AGGGACCTGG CAGCTCCTGC CCCAGGCTGG CTCCTTTCCT GGTACAGCAT GTAATATTCT 1200
AGGGCAGAAA GGCTGTTCT CTCTCCACC CATGAATATC ATTTTGATGA ACCAGAGCTA 1260
25 GGACGATGTC CCGACGGACA GCTTTAAAAC ACCAGCACAG CCTTGCTGAA AACCCACAGC 1320
TTTAATTAGG TTAATCCAGA AAGGGTTGTC TCTGCTAGAT AGGGAGGTCT GGCCAATCGT 1380
GCCAGGAGCG GAGCTCAGCC TGTAGAGTGC CTCCTCTTGA TCCTACCTTT TCAGGCCCTC 1440
AAGCCATCCA TCTATCCATC CCTCTGTAC CATGCCTTCC TGGCTCCAGG CTGGGGGGAG 1500
GGAGAGCCAA AAGTGGGTCT GATCTGAAGT CTTGCCCTCT CTCAAATGCC TGGGTAGAGG 1560
30 GTAGCACCTT TCAGGGAAAG GGTTAAGAAA TGAAAGACTG GAACGGACAT AATTTTGGTG 1620
TAATGGAAGT AGGGGAGCGA TTAATAGTAA AGGAATTTAC AACATTTT 1668

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Mouse FAST-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

45 Met Ala Ser Gly Trp Asp Leu Ala Ser Thr Tyr Thr Pro Thr Thr Pro
1 5 10 15

Ser Pro Gln Leu Ala Leu Ala Pro Ala Gln Gly Tyr Leu Pro Cys Met
 20 25 30
 Gly Pro Arg Asp Asn Ser Gln Leu Arg Pro Pro Glu Ala Glu Ser Leu
 35 40 45
 5 Ser Lys Thr Pro Lys Arg Arg Lys Lys Arg Tyr Leu Arg His Asp Lys
 50 55 60
 Pro Pro Tyr Thr Tyr Leu Ala Met Ile Ala Leu Val Ile Gln Ala Ala
 65 70 75 80
 10 Pro Phe Arg Arg Leu Lys Leu Ala Gln Val Gln Ala Val Phe Pro Phe
 85 90 95
 Phe Arg Asp Asp Tyr Glu Gly Trp Lys Asp Ser Ile Arg His Asn Leu
 100 105 110
 Ser Ser Asn Arg Cys Phe His Lys Val Pro Lys Asp Pro Ala Lys Pro
 115 120 125
 15 Gln Ala Lys Gly Asn Phe Trp Ala Val Asp Val Ser Leu Ile Pro Ala
 130 135 140
 Glu Ala Leu Arg Leu Gln Asn Thr Ala Leu Cys Arg Arg Trp Gln Asn
 145 150 155 160
 Arg Gly Thr His Arg Ala Phe Ala Lys Asp Leu Ser Pro Tyr Val Leu
 165 170 175
 20 His Gly Gln Pro Tyr Gln Pro Pro Ser Pro Pro Pro Pro Arg Glu
 180 185 190
 Gly Phe Ser Ile Lys Ser Leu Leu Gly Asp Pro Gly Lys Glu Ser Thr
 195 200 205
 25 Trp Pro Gln His Pro Gly Leu Pro Gly Gln Ser Thr Ala Ala Gln Ala
 210 215 220
 Gly Thr Leu Ser Lys Gly Glu Glu Gly Met Gly Thr Gly Pro Ser Ser
 225 230 235 240
 Ser Ser Glu Thr Pro Leu Trp Pro Leu Cys Ser Leu Pro Gly Pro Thr
 245 250 255
 30 Ile Ile Glu Gly Glu Ser Ser Gln Gly Glu Val Ile Arg Pro Ser Pro
 260 265 270
 Val Thr Pro Asp Gln Gly Ser Trp Pro Leu His Leu Leu Glu Asp Ser
 275 280 285
 35 Ala Asp Ser Arg Gly Val Pro Arg Arg Gly Ser Arg Ala Ser Leu Trp
 290 295 300
 Gly Gln Leu Pro Thr Ser Tyr Leu Pro Ile Tyr Thr Pro Asn Val Val
 305 310 315 320
 Met Pro Leu Ala Thr Leu Pro Thr Thr Ser Cys Pro Gln Cys Pro Ser
 325 330 335
 40 Ser Ala Ser Pro Ala Tyr Trp Ser Val Gly Thr Glu Ser Gln Gly Ser
 340 345 350
 Gln Asp Leu Leu Cys Asp Leu Asp Ser Leu Phe Gln Gly Val Pro Pro
 355 360 365
 45 Asn Lys Ser Ile Tyr Asp Val Trp Val Ser His Pro Arg Asp Leu Ala
 370 375 380
 Ala Pro Ala Pro Gly Trp Leu Leu Ser Trp Tyr Ser Met
 385 390 395

(2) INFORMATION FOR SEQ ID NO:18:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(ix) FEATURE:

5 (A) NAME/KEY: Other
(B) LOCATION: 1...1
(D) OTHER INFORMATION: Mouse FAST-1 SID

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

10 Ser Tyr Leu Pro Ile Tyr Thr Pro Asn Val Val Met Pro Leu Ala Thr
1 5 10 15
Leu Pro Thr Thr Ser Cys Pro Gln Cys Pro Ser Ser Ala Ser Pro Ala
20 25 30
15 Tyr Trp Ser Val Gly Thr Glu Ser Gln Gly Ser Gln Asp Leu Leu Cys
35 40 45
Asp Leu Asp Ser Leu Phe Gln Gly Val Pro Pro Asn Lys Ser Ile Tyr
50 55 60
Asp Val Trp Val Ser His Pro Arg Asp Leu Ala Ala Pro Ala Pro Gly
65 70 75 80
20 Trp Leu Leu Ser Trp Tyr Ser Met
85